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RAW SEQUENCE LISTING

DATE: 02/22/2002

PATENT APPLICATION: US/09/994,444

TIME: 08:55:01

Input Set : N:\Crf3\RULE60\09994444.txt

Output Set: N:\CRF3\02222002\I994444.raw

SEQUENCE LISTING

EMULATED

4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: Bates, Elizabeth E.M.

7 de Saint-Vis, Blandine M.

8 Caux, Christophe

9 Lebecque, Serge J.E.

10 Banchereau, Jacques

12 (ii) TITLE OF INVENTION: ISOLATED MAMMALIAN DENDRITIC CELL GENES;

13 RELATED REAGENTS

15 (iii) NUMBER OF SEQUENCES: 12

17 (iv) CORRESPONDENCE ADDRESS:

18 (A) ADDRESSEE: DNAX Research Institute

19 (B) STREET: 901 California Avenue

20 (C) CITY: Palo Alto

21 (D) STATE: California

22 (E) COUNTRY: USA

23 (F) ZIP: 94304-1104

25 (v) COMPUTER READABLE FORM:

26 (A) MEDIUM TYPE: Floppy disk

27 (B) COMPUTER: IBM PC compatible

28 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

29 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

31 (vi) CURRENT APPLICATION DATA:

C--> 32 (A) APPLICATION NUMBER: US/09/994,444

C--> 33 (B) FILING DATE: 27-Nov-2001

39 (C) CLASSIFICATION:

45 (vii) PRIOR APPLICATION DATA:

37 (A) APPLICATION NUMBER: US 08/978,289

38 (B) FILING DATE: 25-NOV-1997

42 (A) APPLICATION NUMBER: US 60/032,767

43 (B) FILING DATE: 11-DEC-1996

46 (A) APPLICATION NUMBER: US 60/031,806

47 (B) FILING DATE: 27-NOV-1996

49 (viii) ATTORNEY/AGENT INFORMATION:

50 (A) NAME: Ching, Edwin P.

51 (B) REGISTRATION NUMBER: 34,090

52 (C) REFERENCE/DOCKET NUMBER: DX0669K1

54 (ix) TELECOMMUNICATION INFORMATION:

55 (A) TELEPHONE: (650)852-9196

56 (B) TELEFAX: (650)496-1204

59 (2) INFORMATION FOR SEQ ID NO: 1:

61 (i) SEQUENCE CHARACTERISTICS:

62 (A) LENGTH: 777 base pairs

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63          (B) TYPE: nucleic acid
64          (C) STRANDEDNESS: single
65          (D) TOPOLOGY: linear
67      (ii) MOLECULE TYPE: cDNA
70      (ix) FEATURE:
71          (A) NAME/KEY: CDS
72          (B) LOCATION: 19..513
75      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
77  GGCCCCCTTGT CTGCAGAG ATG GCT CCC AAT GCT TCC TGC CTC TGT GTG CAT      51
78              Met Ala Pro Asn Ala Ser Cys Leu Cys Val His
79              1          5          10
81  GTC CGT TCC GAG GAA TGG GAT TTA ATG ACC TTT GAT GCC AAC CCA TAT      99
82  Val Arg Ser Glu Glu Trp Asp Leu Met Thr Phe Asp Ala Asn Pro Tyr
83              15          20          25
85  GAC AGC GTG AAA AAA ATC AAA GAA CAT GTC CGG TCT AAG ACC AAG GTT      147
86  Asp Ser Val Lys Lys Ile Lys Glu His Val Arg Ser Lys Thr Lys Val
87              30          35          40
89  CCT GTG CAG GAC CAG GTT CTT TTG CTG GGC TCC AAG ATC TTA AAG CCA      195
90  Pro Val Gln Asp Gln Val Leu Leu Leu Gly Ser Lys Ile Leu Lys Pro
91              45          50          55
93  CGG AGA AGC CTC TCA TCT TAT GGC ATT GAC AAA GAG AAG ACC ATC CAC      243
94  Arg Arg Ser Leu Ser Ser Tyr Gly Ile Asp Lys Glu Lys Thr Ile His
95  60          65          70          75
97  CTT ACC CTG AAA GTG GTG AAG CCC AGT GAT GAG GAG CTG CCC TTG TTT      291
98  Leu Thr Leu Lys Val Lys Pro Ser Asp Glu Glu Leu Pro Leu Phe
99              80          85          90
101 CTT GTG GAG TCA GGT GAT GAG GCA AAG AGG CAC CTC CTC CAG GTG CGA      339
102 Leu Val Glu Ser Gly Asp Glu Ala Lys Arg His Leu Leu Gln Val Arg
103              95          100          105
105 AGG TCC AGC TCA GTG GCA CAA GTG AAA GCA ATG ATC GAG ACT AAG ACG      387
106 Arg Ser Ser Ser Val Ala Gln Val Lys Ala Met Ile Glu Thr Lys Thr
107              110          115          120
109 GGT ATA ATC CCT GAG ACC CAG ATT GTG ACT TGC AAT GGA AAG AGA CTG      435
110 Gly Ile Ile Pro Glu Thr Gln Ile Val Thr Cys Asn Gly Lys Arg Leu
111              125          130          135
113 GAA GAT GGG AAG ATG ATG GCA GAT TAC GGC ATC AGA AAG GGC AAC TTA      483
114 Glu Asp Gly Lys Met Met Ala Asp Tyr Gly Ile Arg Lys Gly Asn Leu
115 140          145          150          155
117 CTC TTC CTG GCA TCT TAT TGT ATT GGA GGG TGACCACCCT GGGGATGGGG      533
118 Leu Phe Leu Ala Ser Tyr Cys Ile Gly Gly
119              160          165
121 TGTTGGCAGG GGTCAAAAAG CTTATTTCCTT TTAATCTCTT ACTCAACGAA CACATCTTCT      593
123 GATGATTTC CAAAATTAAT GAGAATGAGA TGACTAGAGT AAGATTTGGG TGGGATGGGGT      653
125 AGGATGAAGT ATATTGCCCA ACTCTATGTT TCTTTGATTC TAACACAATT AATTAAGTGA      713
127 CATGATTTT ACTAATGTAT TACTGAGACT AGTAAATAAA TTTTAAAGGC AAAATAGAGC      773
129 ATTC      777
132 (2) INFORMATION FOR SEQ ID NO: 2:
134      (i) SEQUENCE CHARACTERISTICS:
135          (A) LENGTH: 165 amino acids

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136          (B) TYPE: amino acid
137          (D) TOPOLOGY: linear
139          (ii) MOLECULE TYPE: protein
141          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
143 Met Ala Pro Asn Ala Ser Cys Leu Cys Val His Val Arg Ser Glu Glu
144   1          5          10          15
146 Trp Asp Leu Met Thr Phe Asp Ala Asn Pro Tyr Asp Ser Val Lys Lys
147          20          25          30
149 Ile Lys Glu His Val Arg Ser Lys Thr Lys Val Pro Val Gln Asp Gln
150          35          40          45
152 Val Leu Leu Leu Gly Ser Lys Ile Leu Lys Pro Arg Arg Ser Leu Ser
153          50          55          60
155 Ser Tyr Gly Ile Asp Lys Glu Lys Thr Ile His Leu Thr Leu Lys Val
156   65          70          75          80
158 Val Lys Pro Ser Asp Glu Glu Leu Pro Leu Phe Leu Val Glu Ser Gly
159          85          90          95
161 Asp Glu Ala Lys Arg His Leu Leu Gln Val Arg Arg Ser Ser Ser Val
162          100          105          110
164 Ala Gln Val Lys Ala Met Ile Glu Thr Lys Thr Gly Ile Ile Pro Glu
165          115          120          125
167 Thr Gln Ile Val Thr Cys Asn Gly Lys Arg Leu Glu Asp Gly Lys Met
168          130          135          140
170 Met Ala Asp Tyr Gly Ile Arg Lys Gly Asn Leu Phe Leu Ala Ser
171 145          150          155          160
173 Tyr Cys Ile Gly Gly
174          165
176 (2) INFORMATION FOR SEQ ID NO: 3:
178   (i) SEQUENCE CHARACTERISTICS:
179       (A) LENGTH: 496 base pairs
180       (B) TYPE: nucleic acid
181       (C) STRANDEDNESS: single
182       (D) TOPOLOGY: linear
184   (ii) MOLECULE TYPE: cDNA
187   (ix) FEATURE:
188       (A) NAME/KEY: CDS
189       (B) LOCATION: 8..493
192   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
194 TACAGAC ATG GCT TCT GTC CGC ACC TGT GTT GTC CGT TCA GAC CAA TGG          49
195   Met Ala Ser Val Arg Thr Cys Val Val Arg Ser Asp Gln Trp
196   1          5          10
198 CGG TTA ATG ACC TTT GAG ACC ACT GAG AAT GAC AAA GTG AAG AAG ATA          97
199 Arg Leu Met Thr Phe Glu Thr Thr Glu Asn Asp Lys Val Lys Lys Ile
200 15          20          25          30
202 AAT GAA CAT ATT AGG TCC CAA ACC AAG GTC TCT GTA CAG GAC CAG ATC          145
203 Asn Glu His Ile Arg Ser Gln Thr Lys Val Ser Val Gln Asp Gln Ile
204          35          40          45
206 CTT CTG CTA GAC TCC AAA ATC CTC AAG CCC CAT CGA AAA TTG TCA TCC          193
207 Leu Leu Leu Asp Ser Lys Ile Leu Lys Pro His Arg Lys Leu Ser Ser
208          50          55          60

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210 TAT GGG ATT GAC AAG GAA ACC ACT ATC CAC CTT ACC CTG AAG GTG GTG      241
211 Tyr Gly Ile Asp Lys Glu Thr Thr Ile His Leu Thr Leu Lys Val Val
212      65      70      75
214 AAG CCC AGT GAT GAA GAG CTG CCC TTG TTT CTG GTG GAG TCC AAA AAC      289
215 Lys Pro Ser Asp Glu Glu Leu Pro Leu Phe Leu Val Glu Ser Lys Asn
216      80      85      90
218 GAG GGG CAA AGG CAC CTC CTC CGA GTT CGA AGA TCC AGC TCA GTG GCC      337
219 Glu Gly Gln Arg His Leu Arg Val Arg Arg Ser Ser Ser Val Ala
220      95      100      105      110
222 CAG GTG AAA GAG ATG ATC GAG AGT GTG ACC TCT GTG ATC CCT AAG AAG      385
223 Gln Val Lys Glu Met Ile Glu Ser Val Thr Ser Val Ile Pro Lys Lys
224      115      120      125
226 CAG GTT GTG AAT TGC AAC GGA AAG AAG CTG GAA GAT GGA AAG ATC ATG      433
227 Gln Val Val Asn Cys Asn Gly Lys Lys Leu Glu Asp Gly Lys Ile Met
228      130      135      140
230 GCT GAC TAC AAC ATC AAG AGT GGC AGT TTG CTC TTT CTG ACA ACA CAC      481
231 Ala Asp Tyr Asn Ile Lys Ser Gly Ser Leu Leu Phe Leu Thr Thr His
232      145      150      155
234 TGC ACT GGG GGA TGA      496
235 Cys Thr Gly Gly
236      160
239 (2) INFORMATION FOR SEQ ID NO: 4:
241 (i) SEQUENCE CHARACTERISTICS:
242 (A) LENGTH: 162 amino acids
243 (B) TYPE: amino acid
244 (D) TOPOLOGY: linear
246 (ii) MOLECULE TYPE: protein
248 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
250 Met Ala Ser Val Arg Thr Cys Val Val Arg Ser Asp Gln Trp Arg Leu
251      1      5      10      15
253 Met Thr Phe Glu Thr Thr Glu Asn Asp Lys Val Lys Lys Ile Asn Glu
254      20      25      30
256 His Ile Arg Ser Gln Thr Lys Val Ser Val Gln Asp Gln Ile Leu Leu
257      35      40      45
259 Leu Asp Ser Lys Ile Leu Lys Pro His Arg Lys Leu Ser Ser Tyr Gly
260      50      55      60
262 Ile Asp Lys Glu Thr Thr Ile His Leu Thr Leu Lys Val Val Lys Pro
263      65      70      75      80
265 Ser Asp Glu Glu Leu Pro Leu Phe Leu Val Glu Ser Lys Asn Glu Gly
266      85      90      95
268 Gln Arg His Leu Leu Arg Val Arg Arg Ser Ser Ser Val Ala Gln Val
269      100      105      110
271 Lys Glu Met Ile Glu Ser Val Thr Ser Val Ile Pro Lys Lys Gln Val
272      115      120      125
274 Val Asn Cys Asn Gly Lys Lys Leu Glu Asp Gly Lys Ile Met Ala Asp
275      130      135      140
277 Tyr Asn Ile Lys Ser Gly Ser Leu Leu Phe Leu Thr Thr His Cys Thr
278      145      150      155      160
280 Gly Gly

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283 (2) INFORMATION FOR SEQ ID NO: 5:

285 (i) SEQUENCE CHARACTERISTICS:

286 (A) LENGTH: 1040 base pairs

287 (B) TYPE: nucleic acid

288 (C) STRANDEDNESS: single

289 (D) TOPOLOGY: linear

291 (ii) MOLECULE TYPE: cDNA

294 (ix) FEATURE:

295 (A) NAME/KEY: CDS

296 (B) LOCATION: 45..767

298 (ix) FEATURE:

299 (A) NAME/KEY: mat_peptide

300 (B) LOCATION: 111..767

303 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

```

305 TTCCTTTCAA ATACACACCC CAACCCGCCC CGGCATACAC AGAA ATG GGG ACT GCG      56
306                                     Met Gly Thr Ala
307                                     -22    -20
309 AGC AGA AGC AAC ATC GCT CGC CAT CTG CAA ACC AAT CTC ATT CTA TTT      104
310 Ser Arg Ser Asn Ile Ala Arg His Leu Gln Thr Asn Leu Ile Leu Phe
311          -15          -10          -5
313 TGT GTC GGT GCT GTG GGC GCC TGT ACT CTC TCT GTC ACA CAA CCG TGG      152
314 Cys Val Gly Ala Val Gly Ala Cys Thr Leu Ser Val Thr Gln Pro Trp
315          1          5          10
317 TAC CTA GAA GTG GAC TAC ACT CAT GAG GCC GTC ACC ATA AAG TGT ACC      200
318 Tyr Leu Glu Val Asp Tyr Thr His Glu Ala Val Thr Ile Lys Cys Thr
319 15          20          25          30
321 TTC TCC GCA ACC GGA TGC CCT TCT GAG CAA CCA ACA TGC CTG TGG TTT      248
322 Phe Ser Ala Thr Gly Cys Pro Ser Glu Gln Pro Thr Cys Leu Trp Phe
323          35          40          45
325 CGC TAC GGT GCT CAC CAG CCT GAG AAC CTG TGC TTG GAC GGG TGC AAA      296
326 Arg Tyr Gly Ala His Gln Pro Glu Asn Leu Cys Leu Asp Gly Cys Lys
327          50          55          60
329 AGT GAG GCA GAC AAG TTC ACA GTG AGG GAG GCC CTC AAA GAA AAC CAA      344
330 Ser Glu Ala Asp Lys Phe Thr Val Arg Glu Ala Leu Lys Glu Asn Gln
331          65          70          75
333 GTT TCC CTC ACT GTA AAC AGA GTG ACT TCA AAT GAC AGT GCA ATT TAC      392
334 Val Ser Leu Thr Val Asn Arg Val Thr Ser Asn Asp Ser Ala Ile Tyr
335          80          85          90
337 ATC TGT GGA ATA GCA TTC CCC AGT GTG CCG GAA GCG AGA GCT AAA CAG      440
338 Ile Cys Gly Ile Ala Phe Pro Ser Val Pro Glu Ala Arg Ala Lys Gln
339 95          100          105          110
341 ACA GGA GGA GGG ACC ACA CTG GTG GTA AGA GAA ATT AAG CTG CTC AGC      488
342 Thr Gly Gly Gly Thr Thr Leu Val Val Arg Glu Ile Lys Leu Leu Ser
343          115          120          125
345 AAG GAA CTG CGG AGC TTC CTG ACA GCT CTT GTA TCA CTG CTC TCT GTC      536
346 Lys Glu Leu Arg Ser Phe Leu Thr Ala Leu Val Ser Leu Leu Ser Val
347          130          135          140
349 TAT GTG ACC GGT GTG TGC GTG GCC TTC ATA CTC CTC TCC AAA TCA AAA      584
350 Tyr Val Thr Gly Val Cys Val Ala Phe Ile Leu Leu Ser Lys Ser Lys

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VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\09994444.txt

Output Set: N:\CRF3\02222002\I994444.raw

L:32 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:33 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]